

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:58:35 ; Search time 60.5 Seconds
(without alignments)
1466.589 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169
Sequence: 1 PAPELIGSPVFLFPKPKD.....MHEALNHVTKSLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Published Applications_AA.*

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22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1168	99.9	218	14	US-10-277-370-2
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4	1168	99.9	218	14	US-10-835-642-4
5	1168	99.9	218	16	US-10-757-863-4
6	1168	99.9	218	17	US-10-982-470-4
7	1168	99.9	219	16	US-10-704-406-7
8	1168	99.9	227	15	US-10-269-695-60
9	1168	99.9	227	15	US-10-435-608-2
10	1168	99.9	227	15	US-10-410-998-60
11	1168	99.9	227	15	US-10-622-108-2

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13	1168	99.9	227	17	US-10-822-231-2	Sequence 2, Appli
14	1168	99.9	227	17	US-10-822-231-43	Sequence 43, Appl
15	1168	99.9	227	17	US-10-822-231-56	Sequence 56, Appl
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17	1168	99.9	228	9	US-09-840-277-2	Sequence 2, Appli
18	1168	99.9	228	10	US-09-847-249A-2	Sequence 2, Appli
19	1168	99.9	228	10	US-09-843-221A-2	Sequence 2, Appli
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ALIGNMENTS

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US-09-813-341-2

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; Sequence 2, Application US/09813341
; Publication No. US20020004587A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Kathy L.
; TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1780R1
; CURRENT APPLICATION NUMBER: US/09/813,341
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/195,819
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-341-2

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Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 PABELGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKT 60
    |||

QY 61 KPREEQVXKTRVYVSVTLVHODMLNGEKYCKVSNALPAPIKRTISKAGQREPOVY 120
    |||
DB 61 KPREEQVXKTRVYVSVTLVHODMLNGEKYCKVSNALPAPIKRTISKAGQREPOVY 120
    |||

QY 121 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 180
    |||
DB 121 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 180
    |||

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DB 181 LTVDKSRWQGNVSCVMHEALHNYTKQSLSPGK 218
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RESULT 2
US-10-277-370-2
; Sequence 2, Application US/10277370
; Publication No. US20030157108A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Glycoprotein Compositions
; FILE REFERENCE: P1877R1
; CURRENT APPLICATION NUMBER: US/10/277,370
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/337,642
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/347,694
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-277-370-2

Query Match          99.9%; Score 1168; DB 14; Length 218;
Best Local Similarity 99.5%; Pred. No. 5.9e-89;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 22, 2005, 12:35:38 ; Search time 30 Seconds
(without alignments)
542,450 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169

Sequence: 1 PAEBLLGGPSVFLPPPKPD.....MHBALNHYTKSLISLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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33	1168	99.9	331	3	US-09-761-413-2	Sequence 2, Appl
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47	1168	99.9	387	3	US-09-131-247-16	Sequence 16, Appl
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49	1168	99.9	389	3	US-09-131-247-14	Sequence 14, Appl
50	1168	99.9	389	4	US-09-784-623-14	Sequence 14, Appl
51	1168	99.9	394	4	US-09-854-864-31	Sequence 31, Appl
52	1168	99.9	396	2	US-08-784-512-3	Sequence 3, Appl
53	1168	99.9	396	3	US-09-176-228-3	Sequence 3, Appl
54	1168	99.9	397	4	US-09-854-864-18	Sequence 18, Appl
55	1168	99.9	398	4	US-09-612-033B-14	Sequence 14, Appl
56	1168	99.9	399	4	US-09-832-659A-2	Sequence 2, Appl
57	1168	99.9	418	4	US-09-832-659A-42	Sequence 42, Appl
58	1168	99.9	423	4	US-09-832-659A-44	Sequence 44, Appl
59	1168	99.9	424	3	US-09-333-593A-8	Sequence 8, Appl
60	1168	99.9	424	5	PCT-US95-0386C-12	Sequence 12, Appl
61	1168	99.9	424	5	PCT-US95-0386C-14	Sequence 14, Appl
62	1168	99.9	437	5	PCT-US96-10043-11	Sequence 11, Appl
63	1168	99.9	442	4	US-08-472-889A-7	Sequence 7, Appl
64	1168	99.9	442	5	PCT-US96-10043-9	Sequence 9, Appl
65	1168	99.9	446	3	US-08-397-411-7	Sequence 7, Appl
66	1168	99.9	446	3	US-09-157-452B-12	Sequence 12, Appl
67	1168	99.9	449	1	US-08-458-516-13	Sequence 13, Appl
68	1168	99.9	452	4	US-09-773-877B-16	Sequence 16, Appl
69	1168	99.9	455	4	US-09-773-877B-22	Sequence 22, Appl
70	1168	99.9	458	4	US-09-773-877B-26	Sequence 26, Appl
71	1168	99.9	459	1	US-08-157-101A-7	Sequence 7, Appl
72	1168	99.9	462	4	US-09-773-877B-18	Sequence 18, Appl
73	1168	99.9	467	4	US-08-030-175-41	Sequence 41, Appl
74	1168	99.9	467	4	US-08-030-175-42	Sequence 42, Appl
75	1168	99.9	475	4	US-09-740-002-27	Sequence 27, Appl
76	1168	99.9	475	4	US-08-378-939-10	Sequence 10, Appl
77	1168	99.9	476	2	US-08-487-550-4	Sequence 4, Appl
78	1168	99.9	476	3	US-08-487-550-12	Sequence 12, Appl
79	1168	99.9	476	3	US-08-487-550-12	Sequence 12, Appl
80	1168	99.9	476	4	US-09-526-098-4	Sequence 4, Appl
81	1168	99.9	476	4	US-09-526-098-12	Sequence 12, Appl
82	1168	99.9	476	4	US-09-583-916-4	Sequence 4, Appl
83	1168	99.9	476	4	US-09-583-916-12	Sequence 12, Appl
84	1168	99.9	478	3	US-08-487-550-8	Sequence 8, Appl
85	1168	99.9	478	3	US-09-526-098-8	Sequence 8, Appl
86	1168	99.9	478	4	US-09-383-916-8	Sequence 8, Appl
87	1168	99.9	482	3	US-09-189-129-2	Sequence 2, Appl
88	1168	99.9	482	4	US-09-824-286-2	Sequence 2, Appl
89	1168	99.9	488	3	US-08-776-511-2	Sequence 2, Appl
90	1168	99.9	497	4	US-09-469-846-6	Sequence 6, Appl
91	1168	99.9	525	4	US-09-469-846-8	Sequence 8, Appl
92	1168	99.9	547	4	US-09-469-846-4	Sequence 4, Appl
93	1168	99.9	557	4	US-09-773-877B-14	Sequence 14, Appl
94	1168	99.9	567	4	US-09-825-561A-16	Sequence 16, Appl
95	1168	99.9	567	4	US-09-773-877B-12	Sequence 12, Appl
96	1168	99.9	567	4	US-09-773-877B-20	Sequence 20, Appl
97	1168	99.9	571	4	US-09-746-359A-53	Sequence 53, Appl
98	1168	99.9	592	4	US-09-313-942-8	Sequence 8, Appl
99	1168	99.9	622	4	US-09-499-846-2	Sequence 2, Appl
100	1168	99.9	680	3	US-08-227-496C-15	Sequence 15, Appl

99	1168	99.9	261	7	ABU64198	Abu64198 Plaemid p
100	1168	99.9	261	8	ADO10509	Ado10509 Kb signal
101	1168	99.9	266	5	ABB77128	Abb77128 Human Crl
102	1168	99.9	266	5	ABB77108	Abb77108 Human Crl
103	1168	99.9	266	5	ABB77115	Abb77115 Human Crl
104	1168	99.9	266	5	ABB77121	Abb77121 Human Crl
105	1168	99.9	267	7	AAE26273	AAe26273 Human cpa
106	1168	99.9	267	7	ADK82716	Adk82716 Anti-beta
107	1168	99.9	268	3	AB16959	Ab16959 Fc-TMP-TM
108	1168	99.9	268	3	ABB73412	Abb73412 Fc-TMP-TM
109	1168	99.9	269	3	AA196531	AAy96531 Human IgG
110	1168	99.9	269	3	AB16960	Ab16960 TMP-TMP-F
111	1168	99.9	269	5	ABB73413	Abb73413 TMP-TMP-F
112	1168	99.9	269	8	ADK82719	Adk82719 Anti-beta
113	1168	99.9	277	8	ADJ52120	Adj52120 CHI delet
114	1168	99.9	277	3	AB16967	Ab16967 Fc-EMP-EM
115	1168	99.9	277	3	AB16966	Ab16966 EMP-BMP-F
116	1168	99.9	277	5	ABB73418	Abb73418 Fc-EMP-EM
117	1168	99.9	277	7	ADR82706	Adr82706 Beta-amy1
118	1168	99.9	281	5	AAE15489	AAe15489 Mouse BCM
119	1168	99.9	281	5	AAU81169	AAu81169 Echistaci
120	1168	99.9	283	5	AAE15488	AAe15488 Human BCM
121	1168	99.9	287	4	AAE47590	AAb47590 Fusion pr
122	1168	99.9	293	6	ABJ38345	Abj38345 TAL1-1 in
123	1168	99.9	293	6	ABJ38344	Abj38344 TAL1-1 in
124	1168	99.9	293	4	ADQ6789	Adq6789 AGP3 pep
125	1168	99.9	302	4	AAE60699	AAe60699 Mouse IgG
126	1168	99.9	302	4	AAE00507	AAe00507 Human BCM
127	1168	99.9	302	7	ADG43717	Adg43717 Human B-c
128	1168	99.9	320	5	AAE22245	AAe22245 Murine Ig
129	1168	99.9	320	6	ABR55865	Ab55865 Human Imm
130	1168	99.9	320	8	ADN49722	Adn49722 Human Imm
131	1168	99.9	329	2	AAE91806	AAe91806 Human Imm
132	1168	99.9	329	8	ADP56386	Adp56386 Human PRO
133	1168	99.9	329	8	ADP56389	Adp56389 Human IgG
134	1168	99.9	329	8	ADP56387	Adp56387 Human IgG
135	1168	99.9	330	4	AAE21960	AAe21960 Human IgG
136	1168	99.9	330	5	ABR81641	Ab81641 Human IgG
137	1168	99.9	330	5	ABR81641	Ab81641 Human IgG
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139	1168	99.9	330	6	ABR71856	Ab71856 Human IgG
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146	1168	99.9	330	7	ADP11389	Adp11389 Anti-OPGL
147	1168	99.9	330	7	ADP11389	Adp11389 Anti-OPGL
148	1168	99.9	330	7	ADP11389	Adp11389 Anti-OPGL
149	1168	99.9	330	7	ADP11389	Adp11389 Anti-OPGL
150	1168	99.9	330	8	ADP11389	Adp11389 Anti-OPGL

ALIGNMENTS

RESULT 1
AAB07475
ID AAB07475 standard; protein; 218 AA.
XX
AC AAB07475;
XX
DT 20-OCT-2000 (first entry)
XX
DE Native IgG Fc region humIgG1 (A allotype).
XX
XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;
KW asthma; LFA-1-mediated disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO20042072-A2.

XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US000973.
XX
PR 15-JAN-1999; 99US-0116023P.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG;
XX
DR WPI; 2000-476035/41.
XX
PT New Fc region-containing polypeptides that have altered effector function
PT to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX
PS Disclosure; Fig 22A; 132pp; English.

CC AAB07474-78 represent native IgG Fc regions. The proteins are used to
CC produce Fc region-containing polypeptides that have altered effector
CC function as a consequence of one or more amino acid modifications in the
CC Fc region. The variant polypeptides are useful for treating cancer,
CC allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1
CC -mediated disorders. Where the polypeptide binds the HER2 receptor, the
CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant
CC tumour characterized by overexpression of the HER2 receptor. Such cancers
CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-
CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer,
CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,
CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland
CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,
CC thyroid cancer, hepatic carcinoma and various types of head and neck
CC cancer
XX
SQ Sequence 218 AA;

Query Match 99.9%; Score 1168; DB 3; Length 218;
Best Local Similarity 99.5%; Pred. No. 1e-87; 1; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PABELGSPVFLFPPEKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKT 60
DB 1 PABELGSPVFLFPPEKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKT 60
QY 61 KPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPOVY 120
DB 61 KPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPOVY 120
QY 121 TLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSDGSFFLYSK 180
DB 121 TLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLDSDGSFFLYSK 180
QY 181 LTVDKSRWQGNVFCSCVMHEALHNYTQKSLSLSPGK 218
DB 181 LTVDKSRWQGNVFCSCVMHEALHNYTQKSLSLSPGK 218

RESULT 2
AAB76422
ID AAB76422 standard; protein; 218 AA.
XX
AC AAB76422;
XX
DT 10-APR-2001 (first entry)
XX
DE Human IgG1 A allotype Fc region amino acid sequence.
XX
XX Human; erBB2; HER2; cancer; nervous system disease; stroke; ischaemia;
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
XX

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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:26:52 ; Search time 112.5 Seconds
(without alignments)
992.296 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
Sequence: 1 PABPILGSPVFLFPPKPKD.....MHEALNNHYOKSLISPSGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: UniProt_03.*
2: uniprot_sprot.*
3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	348	2	Q6PYX1
2	1168	99.9	473	2	Q6MZV7
3	1168	99.9	478	2	Q6P181
4	1168	99.9	480	2	Q6P181
5	1162	99.4	330	1	GCL_HUMAN
6	1162	99.4	465	2	Q6GMX6
7	1162	99.4	466	2	Q6IN78
8	1162	99.4	469	2	Q7Z7P5
9	1162	99.4	470	2	Q6P184
10	1162	99.4	470	2	Q7Z5W1
11	1162	99.4	472	2	Q6N089
12	1162	99.4	475	2	Q6GMW7
13	1162	99.4	476	2	Q6GMX1
14	1162	99.4	679	2	Q6PQ08
15	1158	99.1	473	2	Q6P055
16	1158	99.1	475	2	Q6MZ06
17	1158	99.1	480	2	Q6N094
18	1158	99.1	481	2	Q6N097
19	1158	99.1	482	2	Q7Z351
20	1157	99.0	487	2	Q6S2L2
21	1155	98.8	466	2	Q6N096
22	1151	98.5	475	2	Q6N095
23	1151	98.5	544	2	Q6P185
24	1124	96.2	354	2	Q6BT12
25	1124	96.2	518	2	Q6N030
26	1120	95.8	521	2	Q6N4Y9
27	1113	95.2	327	1	GCL_HUMAN
28	1113	95.2	473	1	Q6TFC3
29	1112.5	95.2	326	1	GCL_HUMAN
30	1112.5	95.2	417	2	Q6N093
31	1109.5	94.9	464	2	Q6MZ06

32	1109	94.9	509	2	Q6N177	Q6N177	homo sapien
33	1107.5	94.7	465	2	Q6P6C4	Q6P6C4	homo sapien
34	1104	94.4	220	1	GCL_HUMAN	P01860	homo sapien
35	1104	94.4	476	2	Q6MZV7	Q6MZV7	homo sapien
36	1098.5	94.0	493	2	Q6N094	Q6N094	homo sapien
37	893	76.4	323	1	GCL_HUMAN	P01870	homo sapien
38	875	74.9	337	2	Q6N094	Q6N094	homo sapien
39	853	73.0	329	1	GCL_HUMAN	P01862	homo sapien
40	836	71.5	470	2	Q6N094	Q6N094	homo sapien
41	825	70.6	303	1	GCL_HUMAN	P01862	homo sapien
42	825	70.6	303	1	GCL_HUMAN	P01862	homo sapien
43	825	70.6	303	1	GCL_HUMAN	P01862	homo sapien
44	818.5	70.0	453	2	Q6N094	Q6N094	homo sapien
45	817.5	69.9	458	2	Q6N094	Q6N094	homo sapien
46	816	69.8	326	1	GCL_HUMAN	P01862	homo sapien
47	815	69.7	333	1	GCL_HUMAN	P01862	homo sapien
48	807.5	69.1	324	1	GCL_HUMAN	P01862	homo sapien
49	805	68.9	329	1	GCL_HUMAN	P01862	homo sapien
50	802.5	68.6	333	1	GCL_HUMAN	P01862	homo sapien
51	790	67.6	330	1	GCL_HUMAN	P01862	homo sapien
52	790	67.6	330	1	GCL_HUMAN	P01862	homo sapien
53	786	67.2	464	2	Q6P185	Q6P185	homo sapien
54	786	67.2	464	2	Q6P185	Q6P185	homo sapien
55	786	67.2	464	2	Q6P185	Q6P185	homo sapien
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57	785	67.2	339	1	GCL_HUMAN	P01862	homo sapien
58	784	67.1	332	1	GCL_HUMAN	P01862	homo sapien
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67	358	30.6	454	2	Q6N094	Q6N094	homo sapien
68	358	30.6	454	2	Q6N094	Q6N094	homo sapien
69	358	30.6	454	2	Q6N094	Q6N094	homo sapien
70	358	30.6	454	2	Q6N094	Q6N094	homo sapien
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72	356	30.5	391	1	MUCB_HUMAN	P01855	homo sapien
73	355	30.4	429	1	EPC_RAT	P01855	homo sapien
74	354.5	30.3	585	2	Q6P185	Q6P185	homo sapien
75	354	30.3	421	1	EPC_MOUSE	P01855	homo sapien
76	348.5	29.8	584	2	Q6N094	Q6N094	homo sapien
77	348	29.8	595	2	Q6N094	Q6N094	homo sapien
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82	344	29.4	428	1	EPC_HUMAN	P01855	homo sapien
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92	313	26.8	588	2	Q6N094	Q6N094	homo sapien
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95	313	26.8	588	2	Q6N094	Q6N094	homo sapien
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98	287.5	23.6	446	1	MUCB_HUMAN	P01855	homo sapien
99	278.5	23.8	299	1	ALC_RABIT	P23087	homo sapien
100	278	23.4	430	1	HVC1_HETFR	P23084	homo sapien
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103	267	22.5	393	1	HVC1_HETFR	P23084	homo sapien
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106 258.5 22.1 492 2 072374 072374 homo sapien
107 256.5 21.9 340 1 ALC2_HUMAN ALC2_HUMAN
108 256.5 21.9 416 2 09NP6 09NP6 homo sapien
109 256.5 21.9 477 2 06GMX7 06GMX7 homo sapien
110 256.5 21.9 478 2 06NYH3 06NYH3 homo sapien
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113 256.5 21.9 483 2 06MZ9 06MZ9 homo sapien
114 256.5 21.9 487 2 06ZVX0 06ZVX0 homo sapien
115 256 21.9 353 1 ALC1_HUMAN ALC1_HUMAN
116 256 21.9 384 2 09UP60 09UP60 homo sapien
117 256 21.9 493 2 08NCL6 08NCL6 homo sapien
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123 255.5 21.9 498 2 06N041 06N041 homo sapien
124 255.5 21.9 500 2 06N091 06N091 homo sapien
125 254.5 21.8 353 1 ALC1_GORGO P20758 gorilla gor
126 253 21.6 494 2 06ZM64 06ZM64 homo sapien
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128 253 21.6 499 2 08NSK4 08NSK4 homo sapien
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131 251 21.5 500 2 09BRV0 09BRV0 homo sapien
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136 242.5 20.7 482 2 08K172 08K172 mus musculu
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141 242.5 20.7 488 2 091MR1 091MR1 mus musculu
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144 239.5 20.5 344 1 ALC_MOUSE P01878 mus musculu
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146 239.5 20.5 479 2 07TMK4 07TMK4 mus musculu
147 239.5 20.5 480 2 091X61 091X61 mus musculu
148 239.5 20.5 480 2 08K0Z4 08K0Z4 mus musculu
149 239.5 20.5 481 2 08VCV5 08VCV5 mus musculu
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ALIGNMENTS

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RESULT 1
ID 06PYX1 PRELIMINARY; PRT; 348 AA.
AC 06PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -.
DR HSSP; P01857; IAD7.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.

```

```

DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0B5E845 CRC64;

```

```

Query Match 99.9%; Score 1168; DB 2; Length 348;
Best Local Similarity 99.5%; Pred. No. 2.7e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 PAPERLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 131 PAPERLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 190
QY 61 KPREQYNNXYRVVSVLTVLHQMNLNGEKYCKVSNKALPAPIKTSKAKGPREEPOVY 120
DB 191 KPREQYNNXYRVVSVLTVLHQMNLNGEKYCKVSNKALPAPIKTSKAKGPREEPOVY 250
QY 121 TLPPSRREMTKNQVSLTCLVNGFYPSDIAVWESNGQPENNYKTPPLVDSGSFFLYSK 180
DB 251 TLPPSRREMTKNQVSLTCLVNGFYPSDIAVWESNGQPENNYKTPPLVDSGSFFLYSK 310
QY 181 LTVDKSRWQGNVFSQSVHEALHNHYTQKSLSLSPGK 218
DB 311 LTVDKSRWQGNVFSQSVHEALHNHYTQKSLSLSPGK 348

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RESULT 2

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ID 06MZV7 PRELIMINARY; PRT; 473 AA.
AC 06MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloecher H., Boecher M., Nemes H.W., Weil B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein_
KW SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

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Query Match 99.9%; Score 1168; DB 2; Length 473;
Best Local Similarity 99.5%; Pred. No. 3.9e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 PAPERLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 256 PAPERLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 315

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2005, 12:31:08 ; Search time 25 Seconds
(without alignments)
839,010 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
Sequence: 1 PABPLLGGPSVFLPPPKKD.....MREALNNHYTKSLSPGK 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	374	2 S69339	Ig heavy chain V r
2	1162	99.4	255	4 S31866	Ig gamma-1 chain C
3	1162	99.4	330	1 GHMU	Ig gamma-1 chain C
4	1124	96.2	377	2 A23511	Ig gamma-3 chain C
5	1122	96.0	377	2 A60764	Ig gamma-3 chain C
6	1116	95.5	234	1 PT0207	Ig gamma-4 chain C
7	1113	95.2	327	1 G4HU	Ig gamma-4 chain C
8	1112.5	95.2	326	1 G2HU	Ig gamma-2 chain C
9	1099	94.0	289	1 G3HUI	Ig gamma-3 heavy C
10	893	76.4	323	1 GHRB	Ig gamma chain C r
11	883	75.5	328	2 I47160	Ig gamma-2b chain
12	883	75.5	328	2 I47159	Ig gamma-2a chain
13	877	75.0	277	2 I47162	Ig gamma-4 chain C
14	857	73.3	328	2 I47158	Ig gamma-1 chain C
15	855	73.1	328	2 I47161	Ig gamma-3 chain C
16	853	73.0	329	1 G2GP	Ig gamma-2 chain C
17	836	71.5	329	1 G3MSC	Ig gamma-3 chain C
18	836	71.5	470	2 S22080	Ig heavy chain pre
19	832	71.2	308	2 C30554	Ig heavy chain C r
20	832	71.2	472	2 S31459	Ig gamma-1 chain C
21	825	70.6	398	1 G3MSM	Ig gamma-3 chain C
22	817.5	69.9	444	2 PC4436	monoclonal antibody
23	816	69.8	326	2 PS0017	Ig gamma-1 chain C
24	815	69.7	332	2 PS0018	Ig gamma-2b chain
25	807.5	69.1	324	1 G1MS	Ig gamma-1 chain C
26	806	68.9	329	2 S00847	Ig gamma-2c chain
27	802.5	68.6	393	1 G1MSM	Ig gamma-1 chain C
28	790	67.6	330	1 G2MSA	Ig gamma-2a chain
29	790	67.6	469	2 S37483	Ig gamma-2a chain

30	785	67.2	399	1 G2MSAM	Ig gamma-2a chain
31	784	67.1	322	2 PS0019	Ig gamma-2a chain
32	782	66.9	335	1 G2MSAB	Ig gamma-2a chain
33	775	66.3	446	2 S40295	Ig gamma-2a chain
34	761	65.1	327	2 S06611	Ig gamma-2 chain C
35	757	64.8	474	1 G2MS11	Ig gamma-2b chain
36	752	64.3	405	1 G2MSBM	Ig gamma-2b chain
37	735	62.9	475	2 S01321	Ig gamma-2b chain
38	704	60.2	180	2 I46732	Ig gamma heavy cha
39	582.5	49.8	249	2 S69340	Ig heavy chain VHI
40	573	49.0	152	2 S14236	Ig gamma-1 chain C
41	568.5	48.6	218	2 A36040	Ig heavy chain V-I
42	395	33.8	572	2 B46529	Ig heavy chain (
43	358	30.6	453	1 S37768	Ig mu chain C regi
44	356	30.5	391	2 MHHUBT	Ig mu heavy chain
45	355.5	30.4	448	2 S03186	Ig heavy chain C r
46	355	30.4	429	1 EHRT	Ig epsilon chain C
47	354	30.3	388	1 EHMS	Ig epsilon chain C
48	351	30.0	548	2 S38864	Ig epsilon chain C
49	350.5	30.0	549	2 S04845	Ig heavy chain pre
50	349.5	29.9	452	1 MHHU	Ig mu chain C regi
51	348	29.8	627	2 S14683	Ig mu chain precu
52	347	29.7	433	2 S25644	Ig mu chain C regi
53	346	29.6	455	1 MMS	Ig mu chain C regi
54	346	29.6	455	2 A24976	Ig mu chain C regi
55	345	29.5	426	2 I36948	Ig epsilon-chain -
56	345	29.5	474	2 S15590	Ig heavy chain - h
57	344	29.4	428	1 EHHU	Ig epsilon chain C
58	339.5	29.0	473	1 MHHUM	Ig mu chain C regi
59	337.5	28.9	504	2 S00390	Ig gamma chain (c1
60	336	28.7	458	1 MHRB	Ig mu chain C regi
61	336	28.7	476	1 MMSM	Ig mu chain C regi
62	332.5	28.4	423	1 EHMS	Ig epsilon chain C
63	332	28.4	450	1 MHDG	Ig mu chain C regi
64	328	28.1	454	1 MHHY	Ig mu chain C regi
65	327.5	28.0	112	2 B30503	Ig gamma-2a chain
66	326	27.9	479	1 MHRBM	Ig mu chain C regi
67	323	27.6	457	2 S03961	Ig mu chain C regi
68	322	27.5	592	2 S25705	Ig mu chain - bhee
69	313	26.8	453	2 C31933	Ig mu chain C regi
70	296	25.3	577	2 I50731	Ig heavy chain - n
71	295.5	25.3	433	2 S31436	Ig epsilon chain -
72	291	24.9	438	1 HVRK2	Ig mu chain C regi
73	289.5	24.8	342	2 I47175	Ig alpha chain C r
74	287.5	24.6	367	1 MHC	Ig mu chain C regi
75	278.5	23.8	299	1 AHRB	Ig alpha chain C r
76	278	23.8	343	2 S09272	Ig mu chain C regi
77	278	23.8	438	1 HVRKCS	Ig mu chain C regi
78	274	23.4	370	1 HVRKS	Ig mu chain C regi
79	273.5	23.4	585	2 A46507	Ig alpha chain - C
80	272.5	23.3	388	2 S09276	Ig alpha chain C r
81	271.5	23.2	88	2 A30503	Ig gamma-2b chain
82	269	23.0	461	1 HVRKC0	Ig mu chain C regi
83	268.5	23.0	339	2 S09264	Ig alpha chain C r
84	267	22.8	357	2 S09269	Ig mu chain C regi
85	267	22.8	393	1 HVRK1	Ig heavy chain C r
86	263.5	22.5	244	2 S12328	Ig heavy chain C r
87	263.5	22.5	684	2 S60266	novel antigen rece
88	263	22.5	111	2 S43148	Ig epsilon chain -
89	261.5	22.4	357	2 S09265	Ig alpha chain C r
90	259.5	22.2	348	2 S09270	Ig alpha chain C r
91	259.5	22.2	352	2 S09266	Ig mu chain - Lepi
92	257.5	22.0	474	2 I50830	Ig alpha-2 chain -
93	256.5	21.9	340	2 I56230	Ig alpha-2 chain C
94	256.5	21.9	340	2 B23360	Ig alpha-2 chain C
95	256.5	21.9	347	2 S09274	Ig alpha chain C r
96	256	21.9	353	1 AIHU	Ig alpha-1 chain C
97	254.5	21.8	352	2 S05500	Ig alpha-1 chain C
98	253.5	21.7	454	2 A46532	Ig mu chain C regi
99	253	21.6	568	2 S09271	Ig alpha chain C r
100	253	21.6	568	2 A34891	Ig heavy chain pre
101	250.5	21.4	348	2 S09273	Ig alpha chain C r
102	247.5	21.2	340	1 AZHU	Ig alpha-2 chain C

103 247 21.1 342 2 A45966 Ig alpha chain C r
104 246.5 21.1 568 2 A45804 Ig mu chain C regi
105 246 21.0 220 2 C22360 Ig lambda-2 chain C
106 246 21.0 357 2 S09267 Ig alpha chain C r
107 245 21.0 573 2 S12838 Ig mu chain precu
108 239.5 20.5 344 1 AHMS Ig alpha chain C r
109 231.5 19.8 335 2 S09275 Ig alpha chain C r
110 231 19.8 580 2 A46538 Ig heavy chain, se
111 227 19.4 358 2 S09268 Ig alpha chain C r
112 212 18.1 115 2 I68731 IGE chain C4 regio
113 209 17.9 448 2 A46533 Ig heavy chain C r
114 206 17.6 402 2 S20002 Ig heavy chain, se
115 205 17.5 115 2 I68727 IGB chain C4 regio
116 202 17.3 228 2 S03050 Ig gamma chain C r
117 186.5 16.0 140 2 A34509 Ig light chain C r
118 184.5 15.8 106 2 S22760 Ig lambda-2 chain
119 184.5 15.8 214 2 PC4156 Ig lambda chain V
120 183 15.7 212 2 S70431 Ig lambda chain -
121 181 15.5 231 2 S25751 Ig heavy chain -
122 181 15.5 1005 2 T18537 Ig lambda chain (K
123 180 15.4 216 2 S03401 SHP substrate-1 pr
124 180 15.4 509 2 JCS288 SHP substrate-1 pr
125 180 15.4 513 2 JCS289 SHP substrate-1 pr
126 179.5 15.4 233 2 I51383 Ig lambda chain -
127 179.5 15.4 240 2 A41797 Ig light chain - s
128 179 15.3 105 2 B27390 Ig lambda-2 chain
129 178.5 15.3 105 1 LIMS Ig lambda-1 chain
130 178 15.2 118 2 A46516 Ig lambda chain C
131 176 15.1 102 2 B34509 Ig light chain C r
132 176 15.1 118 2 A39949 Ig lambda chain J-
133 175 15.0 227 2 PH1215 Ig epsilon chain C
134 175 15.0 243 2 PH1216 Ig epsilon chain C
135 174 14.9 232 2 S25756 Ig lambda chain -
136 174 14.9 235 2 S25750 Ig lambda chain -
137 173 14.8 118 2 C46516 Ig lambda chain C
138 172 14.7 118 2 S12440 Ig lambda chain (M
139 172 14.7 235 2 S25754 Ig lambda chain -
140 172 14.7 235 2 S25758 Ig lambda chain -
141 171.5 14.7 118 2 B30505 Ig lambda-6 chain
142 171.5 14.7 232 2 S17399 Ig lambda chain pr
143 171 14.6 118 2 S12443 Ig lambda chain (K
144 170 14.5 105 2 S27632 Ig lambda-2 chain
145 170 14.5 231 2 S25738 Ig lambda chain -
146 169.5 14.5 234 2 S25757 Ig lambda chain -
147 169 14.5 115 2 E53116 Ig epsilon chain C
148 169 14.5 235 2 S05270 Ig lambda chain pr
149 168.5 14.4 231 2 PC4155 Ig gamma-2b chain
150 168 14.4 105 2 S22759 Ig lambda-2 chain

ALIGNMENTS

RESULT 1
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khanlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; M0ID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khanlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
C:Accession: S72664
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.9%; Score 1168; DB 2; Length 374;
Best Local Similarity 99.5%; Pred. No. 5.86-86;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 157 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 216
QY 61 KPREEQYNTYRVVSVLTFLHQMNLNGKEYCKVSNKALPAPIETKISKAKGPREPQVY 120
DB 217 KPREEQYNTYRVVSVLTFLHQMNLNGKEYCKVSNKALPAPIETKISKAKGPREPQVY 276
QY 121 TLPPREEMTKNQVSLTCLVKGYFPPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
DB 277 TLPPREEMTKNQVSLTCLVKGYFPPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 336
QY 181 LTVDSRWQOGNVFSCSYMEHALNHYTKSLSPGK 218
DB 337 LTVDSRWQOGNVFSCSYMEHALNHYTKSLSPGK 374

RESULT 2
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C>Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FTL>
A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069
C:Keywords: Immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 99.4%; Score 1162; DB 4; Length 255;
Best Local Similarity 98.6%; Pred. No. 1.1e-85;
Matches 215; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 38 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 97
QY 61 KPREEQYNTYRVVSVLTFLHQMNLNGKEYCKVSNKALPAPIETKISKAKGPREPQVY 120
DB 98 KPREEQYNTYRVVSVLTFLHQMNLNGKEYCKVSNKALPAPIETKISKAKGPREPQVY 157
QY 121 TLPPREEMTKNQVSLTCLVKGYFPPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
DB 158 TLPPREEMTKNQVSLTCLVKGYFPPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 217
QY 181 LTVDSRWQOGNVFSCSYMEHALNHYTKSLSPGK 218
DB 218 LTVDSRWQOGNVFSCSYMEHALNHYTKSLSPGK 255

RESULT 3
GHNU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2005, 12:58:35 ; Search time 60.5 Seconds
(without alignments)
1466.589 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169

Sequence: 1 PAPERLGGPSVFLPPPKKD.....MHEALHNYTKSLSLSPGK 218

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	218	9	US-09-813-341-1
2	1168	99.9	218	14	US-10-277-370-1
3	1168	99.9	218	14	US-10-196-394-72
4	1168	99.9	218	15	US-10-370-749-15
5	1168	99.9	218	16	US-10-835-642-3
6	1168	99.9	218	16	US-10-757-863-3
7	1168	99.9	218	17	US-10-982-470-3
8	1168	99.9	223	14	US-10-135-636-3
9	1168	99.9	228	17	US-10-399-093-5
10	1168	99.9	232	9	US-09-977-034-4
11	1168	99.9	232	14	US-10-071-459A-15

12	1168	99.9	232	14	US-10-292-418-2	Sequence 2, Appli
13	1168	99.9	232	14	US-10-020-354-83	Sequence 83, Appli
14	1168	99.9	232	15	US-10-466-593-2	Sequence 2, Appli
15	1168	99.9	232	15	US-10-419-058-6	Sequence 6, Appli
16	1168	99.9	232	17	US-10-953-259-4	Sequence 4, Appli
17	1168	99.9	264	15	US-10-433-108-18	Sequence 18, Appli
18	1168	99.9	264	15	US-10-433-108-20	Sequence 20, Appli
19	1168	99.9	272	15	US-10-433-108-19	Sequence 19, Appli
20	1168	99.9	272	15	US-10-433-108-21	Sequence 21, Appli
21	1168	99.9	272	15	US-10-433-108-22	Sequence 22, Appli
22	1168	99.9	272	15	US-10-433-108-29	Sequence 29, Appli
23	1168	99.9	272	15	US-10-433-108-30	Sequence 30, Appli
24	1168	99.9	280	15	US-10-433-108-27	Sequence 27, Appli
25	1168	99.9	287	15	US-10-433-108-28	Sequence 28, Appli
26	1168	99.9	287	15	US-10-433-108-23	Sequence 23, Appli
27	1168	99.9	287	15	US-10-433-108-31	Sequence 31, Appli
28	1168	99.9	294	15	US-10-433-108-32	Sequence 32, Appli
29	1168	99.9	302	15	US-10-433-108-25	Sequence 25, Appli
30	1168	99.9	329	15	US-10-370-749-25	Sequence 25, Appli
31	1168	99.9	329	16	US-10-426-334-1	Sequence 1, Appli
32	1168	99.9	330	9	US-09-301-593-22	Sequence 22, Appli
33	1168	99.9	330	14	US-10-121-464-20	Sequence 20, Appli
34	1168	99.9	330	14	US-10-159-006-22	Sequence 20, Appli
35	1168	99.9	330	15	US-10-366-709-52	Sequence 52, Appli
36	1168	99.9	330	16	US-10-688-925-53	Sequence 53, Appli
37	1168	99.9	330	16	US-10-741-481-45	Sequence 45, Appli
38	1168	99.9	330	17	US-10-901-735-3	Sequence 3, Appli
39	1168	99.9	330	17	US-10-706-689-2	Sequence 2, Appli
40	1168	99.9	330	18	US-10-988-360-2	Sequence 2, Appli
41	1168	99.9	334	16	US-10-424-986-28	Sequence 28, Appli
42	1168	99.9	367	16	US-10-424-986-26	Sequence 26, Appli
43	1168	99.9	397	8	US-08-779-457-47	Sequence 47, Appli
44	1168	99.9	397	17	US-10-921-710-47	Sequence 4, Appli
45	1168	99.9	397	17	US-10-491-997-16	Sequence 16, Appli
46	1168	99.9	399	9	US-09-859-361-7	Sequence 7, Appli
47	1168	99.9	401	9	US-09-859-361-9	Sequence 9, Appli
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49	1168	99.9	408	9	US-09-854-208-12	Sequence 12, Appli
50	1168	99.9	425	9	US-09-854-280-13	Sequence 13, Appli
51	1168	99.9	425	9	US-09-854-208-13	Sequence 13, Appli
52	1168	99.9	443	14	US-10-053-302-23	Sequence 23, Appli
53	1168	99.9	447	16	US-10-379-392-116	Sequence 116, Appli
54	1168	99.9	448	15	US-10-467-546-4	Sequence 4, Appli
55	1168	99.9	448	17	US-10-666-332-4	Sequence 4, Appli
56	1168	99.9	449	14	US-10-323-268-23	Sequence 23, Appli
57	1168	99.9	449	16	US-10-318-397-22	Sequence 22, Appli
58	1168	99.9	449	16	US-10-317-747-22	Sequence 22, Appli
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66	1168	99.9	450	9	US-09-796-848A-51	Sequence 51, Appli
67	1168	99.9	450	9	US-09-796-848A-53	Sequence 53, Appli
68	1168	99.9	450	9	US-09-996-288-208	Sequence 208, Appli
69	1168	99.9	450	9	US-09-996-288-210	Sequence 210, Appli
70	1168	99.9	450	9	US-09-996-288-212	Sequence 212, Appli
71	1168	99.9	450	9	US-09-996-288-214	Sequence 214, Appli
72	1168	99.9	450	9	US-09-996-288-216	Sequence 216, Appli
73	1168	99.9	450	9	US-09-996-288-218	Sequence 218, Appli
74	1168	99.9	450	9	US-09-996-288-220	Sequence 220, Appli
75	1168	99.9	450	9	US-09-996-288-222	Sequence 222, Appli
76	1168	99.9	450	9	US-09-996-288-224	Sequence 224, Appli
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87	1168	99.9	450	9	US-09-996-288-248	Sequence 248, App
88	1168	99.9	450	9	US-09-996-288-250	Sequence 250, App
89	1168	99.9	450	9	US-09-996-288-252	Sequence 252, App
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91	1168	99.9	450	9	US-09-996-288-256	Sequence 256, App
92	1168	99.9	450	10	US-09-996-285-208	Sequence 208, App
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100	1168	99.9	450	10	US-09-996-285-224	Sequence 224, App
101	1168	99.9	450	10	US-09-996-285-226	Sequence 226, App
102	1168	99.9	450	10	US-09-996-285-228	Sequence 228, App
103	1168	99.9	450	10	US-09-996-285-232	Sequence 232, App
104	1168	99.9	450	10	US-09-996-285-234	Sequence 234, App
105	1168	99.9	450	10	US-09-996-285-236	Sequence 236, App
106	1168	99.9	450	10	US-09-996-285-238	Sequence 238, App
107	1168	99.9	450	10	US-09-996-285-240	Sequence 240, App
108	1168	99.9	450	10	US-09-996-285-242	Sequence 242, App
109	1168	99.9	450	10	US-09-996-285-244	Sequence 244, App
110	1168	99.9	450	10	US-09-996-285-246	Sequence 246, App
111	1168	99.9	450	10	US-09-996-285-248	Sequence 248, App
112	1168	99.9	450	10	US-09-996-285-250	Sequence 250, App
113	1168	99.9	450	10	US-09-996-285-252	Sequence 252, App
114	1168	99.9	450	10	US-09-996-285-254	Sequence 254, App
115	1168	99.9	450	10	US-09-996-285-256	Sequence 256, App
116	1168	99.9	450	14	US-10-135-636-1	Sequence 1, Appli
117	1168	99.9	450	17	US-10-900-230-208	Sequence 208, App
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122	1168	99.9	450	17	US-10-900-230-218	Sequence 218, App
123	1168	99.9	450	17	US-10-900-230-220	Sequence 220, App
124	1168	99.9	450	17	US-10-900-230-222	Sequence 222, App
125	1168	99.9	450	17	US-10-900-230-224	Sequence 224, App
126	1168	99.9	450	17	US-10-900-230-226	Sequence 226, App
127	1168	99.9	450	17	US-10-900-230-228	Sequence 228, App
128	1168	99.9	450	17	US-10-900-230-232	Sequence 232, App
129	1168	99.9	450	17	US-10-900-230-234	Sequence 234, App
130	1168	99.9	450	17	US-10-900-230-236	Sequence 236, App
131	1168	99.9	450	17	US-10-900-230-238	Sequence 238, App
132	1168	99.9	450	17	US-10-900-230-240	Sequence 240, App
133	1168	99.9	450	17	US-10-900-230-242	Sequence 242, App
134	1168	99.9	450	17	US-10-900-230-244	Sequence 244, App
135	1168	99.9	450	17	US-10-900-230-246	Sequence 246, App
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137	1168	99.9	450	17	US-10-900-230-250	Sequence 250, App
138	1168	99.9	450	17	US-10-900-230-252	Sequence 252, App
139	1168	99.9	450	17	US-10-900-230-254	Sequence 254, App
140	1168	99.9	450	17	US-10-900-230-256	Sequence 256, App
141	1168	99.9	450	18	US-10-962-285-208	Sequence 208, App
142	1168	99.9	450	18	US-10-962-285-210	Sequence 210, App
143	1168	99.9	450	18	US-10-962-285-212	Sequence 212, App
144	1168	99.9	450	18	US-10-962-285-214	Sequence 214, App
145	1168	99.9	450	18	US-10-962-285-216	Sequence 216, App
146	1168	99.9	450	18	US-10-962-285-218	Sequence 218, App
147	1168	99.9	450	18	US-10-962-285-220	Sequence 220, App
148	1168	99.9	450	18	US-10-962-285-222	Sequence 222, App
149	1168	99.9	450	18	US-10-962-285-224	Sequence 224, App
150	1168	99.9	450	18	US-10-962-285-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-09-813-341-1

				Sequence 1, Application US/09813341
				Publication No. US20020004587A1
				GENERAL INFORMATION:
				APPLICANT: Miller, Kathy L.
				APPLICANT: Presta, Leonard G.
				TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
				FILE REFERENCE: P1780R1
				CURRENT APPLICATION NUMBER: US/09/813,341
				CURRENT FILING DATE: 2001-03-20
				PRIOR APPLICATION NUMBER: US 60/195,819
				PRIOR FILING DATE: 2000-04-11
				NUMBER OF SEQ ID NOS: 11
				SEQ ID NO 1
				LENGTH: 218
				TYPE: PRT
				ORGANISM: Homo sapiens
				US-09-813-341-1
QY		Query Match	99.9%; Score 1168; DB 9; Length 218;	
		Best Local Similarity	99.5%; Pred. No. 6e-89;	
		Matches 217; Conservative	0; Mismatches 1; Indels 0; Gaps 0	
Db	1	PAPBLLGSPSVFLPPEPKDXTLMSRTPETVCVVVDVSHEDPEYKFNMTYDGVYHNAKT	60	
QY	1	PAPBLLGSPSVFLPPEPKDXTLMSRTPETVCVVVDVSHEDPEYKFNMTYDGVYHNAKT	60	
Db	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
QY	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
Db	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
QY	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
Db	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
QY	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
Db	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
QY	181	LTVDKSRWQGNVSCSVMEHAIHNYTKSLSPGK	218	
Db	181	LTVDKSRWQGNVSCSVMEHAIHNYTKSLSPGK	218	
		RESULT 2		
		US-10-277-370-1		
		Sequence 1, Application US/10277370		
		Publication No. US20030157108A1		
		GENERAL INFORMATION:		
		APPLICANT: Presta, Leonard G.		
		TITLE OF INVENTION: Glycoprotein Compositions		
		FILE REFERENCE: P1877R1		
		CURRENT APPLICATION NUMBER: US/10/277,370		
		CURRENT FILING DATE: 2003-02-10		
		PRIOR APPLICATION NUMBER: US 60/337,642		
		PRIOR FILING DATE: 2001-10-25		
		PRIOR APPLICATION NUMBER: US 60/347,694		
		PRIOR FILING DATE: 2002-01-09		
		NUMBER OF SEQ ID NOS: 9		
		SEQ ID NO 1		
		LENGTH: 218		
		TYPE: PRT		
		ORGANISM: homo sapiens		
		US-10-277-370-1		
QY		Query Match	99.9%; Score 1168; DB 14; Length 218;	
		Best Local Similarity	99.5%; Pred. No. 6e-89;	
		Matches 217; Conservative	0; Mismatches 1; Indels 0; Gaps 0	
Db	1	PAPBLLGSPSVFLPPEPKDXTLMSRTPETVCVVVDVSHEDPEYKFNMTYDGVYHNAKT	60	
QY	1	PAPBLLGSPSVFLPPEPKDXTLMSRTPETVCVVVDVSHEDPEYKFNMTYDGVYHNAKT	60	
Db	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
QY	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
Db	61	KPREQVXKTRVYVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGPREPOVY	120	
QY	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
Db	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
QY	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	
Db	121	TLPSREBMTKNQVSLTCLVKGFPYPSDIAVEMESNGOPENNYKTTTPVLDSGSEFLYSK	180	

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OM protein - protein search, using SW model

Run on: September 22, 2005, 12:35:38 ; Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169

Sequence: 1 PABELLGSPFVFLPPKPKD.....MHEALNHVYQKSLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.9	218	4	US-09-483-588-3
2	1168	99.9	330	4	US-09-301-593-22
3	1168	99.9	397	4	US-08-775-066-2
4	1168	99.9	449	3	US-08-897-236-23
5	1168	99.9	449	4	US-09-500-2538-23
6	1168	99.9	450	4	US-09-986-288-208
7	1168	99.9	450	4	US-09-986-288-210
8	1168	99.9	450	4	US-09-986-288-212
9	1168	99.9	450	4	US-09-986-288-214
10	1168	99.9	450	4	US-09-986-288-216
11	1168	99.9	450	4	US-09-986-288-218
12	1168	99.9	450	4	US-09-986-288-220
13	1168	99.9	450	4	US-09-986-288-222
14	1168	99.9	450	4	US-09-986-288-224
15	1168	99.9	450	4	US-09-986-288-226
16	1168	99.9	450	4	US-09-986-288-228
17	1168	99.9	450	4	US-09-986-288-230
18	1168	99.9	450	4	US-09-986-288-232
19	1168	99.9	450	4	US-09-986-288-234
20	1168	99.9	450	4	US-09-986-288-236
21	1168	99.9	450	4	US-09-986-288-238
22	1168	99.9	450	4	US-09-986-288-240
23	1168	99.9	450	4	US-09-986-288-242
24	1168	99.9	450	4	US-09-986-288-244
25	1168	99.9	450	4	US-09-986-288-246
26	1168	99.9	450	4	US-09-986-288-248
27	1168	99.9	450	4	US-09-986-288-250

28	1168	99.9	450	4	US-09-986-288-254	Sequence 254, App
29	1168	99.9	450	4	US-09-986-288-256	Sequence 256, App
30	1168	99.9	451	2	US-08-887-3528-14	Sequence 14, App1
31	1168	99.9	451	2	US-08-887-3528-16	Sequence 16, App1
32	1168	99.9	451	2	US-08-887-3528-18	Sequence 18, App1
33	1168	99.9	451	3	US-08-466-151-65	Sequence 65, App1
34	1168	99.9	451	3	US-09-109-207C-14	Sequence 14, App1
35	1168	99.9	451	3	US-09-109-207C-16	Sequence 16, App1
36	1168	99.9	451	3	US-09-109-207C-18	Sequence 18, App1
37	1168	99.9	451	3	US-09-282-505-2	Sequence 2, App1
38	1168	99.9	451	3	US-09-054-255-2	Sequence 2, App1
39	1168	99.9	451	3	US-09-296-005-14	Sequence 14, App1
40	1168	99.9	451	3	US-09-296-005-16	Sequence 16, App1
41	1168	99.9	451	3	US-09-296-005-18	Sequence 18, App1
42	1168	99.9	451	3	US-09-282-846-2	Sequence 2, App1
43	1168	99.9	451	4	US-09-680-145-2	Sequence 2, App1
44	1168	99.9	451	4	US-09-920-171-14	Sequence 14, App1
45	1168	99.9	451	4	US-09-920-171-16	Sequence 16, App1
46	1168	99.9	451	4	US-09-920-171-18	Sequence 18, App1
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49	1168	99.9	451	4	US-09-716-028-18	Sequence 18, App1
50	1168	99.9	451	4	US-09-483-588-2	Sequence 2, App1
51	1168	99.9	451	4	US-10-113-996-14	Sequence 14, App1
52	1168	99.9	451	4	US-10-113-996-16	Sequence 16, App1
53	1168	99.9	451	4	US-10-113-996-18	Sequence 18, App1
54	1168	99.9	451	4	US-09-986-288-230	Sequence 20, App1
55	1168	99.9	452	3	US-09-027-449-71	Sequence 71, App1
56	1168	99.9	452	3	US-09-026-985-71	Sequence 71, App1
57	1168	99.9	452	3	US-09-121-952A-71	Sequence 71, App1
58	1168	99.9	452	4	US-09-234-340B-71	Sequence 71, App1
59	1168	99.9	453	3	US-08-466-151-8	Sequence 8, App1
60	1168	99.9	453	3	US-08-466-163B-18	Sequence 8, App1
61	1168	99.9	453	4	US-09-301-593-18	Sequence 18, App1
62	1168	99.9	453	4	US-09-802-096-8	Sequence 8, App1
63	1168	99.9	453	4	US-09-802-077-8	Sequence 8, App1
64	1168	99.9	454	2	US-07-934-373C-22	Sequence 22, App1
65	1168	99.9	454	3	US-08-437-642B-22	Sequence 22, App1
66	1168	99.9	454	4	US-08-146-206C-22	Sequence 22, App1
67	1168	99.9	454	4	US-09-705-686-22	Sequence 22, App1
68	1168	99.9	454	4	US-09-705-392A-22	Sequence 22, App1
69	1168	99.9	454	4	US-09-705-398-22	Sequence 22, App1
70	1168	99.9	454	5	PCT-US93-07832-22	Sequence 22, App1
71	1168	99.9	466	4	US-09-698-705-11	Sequence 11, App1
72	1168	99.9	467	4	US-09-049-672A-8	Sequence 8, App1
73	1168	99.9	472	4	US-09-301-593-30	Sequence 30, App1
74	1168	99.9	472	4	US-09-301-593-43	Sequence 43, App1
75	1168	99.9	473	3	US-09-049-672A-8	Sequence 4, App1
76	1168	99.9	631	4	US-09-056-461-22	Sequence 22, App1
77	1168	99.9	664	3	US-08-957-063-16	Sequence 16, App1
78	1168	99.9	664	3	US-08-957-063-18	Sequence 18, App1
79	1168	99.9	664	3	US-09-487-685-16	Sequence 16, App1
80	1168	99.9	664	3	US-08-802-805D-16	Sequence 16, App1
81	1168	99.9	664	3	US-08-802-805D-18	Sequence 18, App1
82	1168	99.9	664	3	US-09-388-316C-16	Sequence 16, App1
83	1168	99.9	664	4	US-09-388-316C-18	Sequence 18, App1
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87	1168	99.9	784	4	US-09-313-942-30	Sequence 30, App1
88	1168	99.9	793	4	US-09-313-942-32	Sequence 32, App1
89	1168	99.9	910	4	US-09-313-942-38	Sequence 38, App1
90	1168	99.9	977	4	US-09-590-656-1	Sequence 1, App1
91	1168	99.9	977	4	US-09-679-397-2	Sequence 2, App1
92	1168	99.9	449	3	US-09-680-148-2	Sequence 2, App1
93	1168	99.9	449	4	US-09-304-465A-2	Sequence 2, App1
94	1168	99.9	449	4	US-09-483-588-4	Sequence 4, App1
95	1168	99.9	449	4	US-09-428-082B-2	Sequence 2, App1
96	1168	99.9	449	4	US-09-840-669B-2	Sequence 2, App1
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104 1162 99.4 232 2 US-08-595-043A-50 Sequence 50, Appli
105 1162 99.4 232 2 US-09-968-362A-26 Sequence 26, Appli
106 1162 99.4 235 3 US-09-131-247-6 Sequence 6, Appli
107 1162 99.4 243 4 US-09-784-623-6 Sequence 6, Appli
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124 1162 99.4 277 4 US-09-428-082B-22 Sequence 22, Appli
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136 1162 99.4 360 3 US-09-180-100-11 Sequence 11, Appli
137 1162 99.4 371 1 US-08-236-311-7 Sequence 7, Appli
138 1162 99.4 371 3 US-08-457-918-7 Sequence 7, Appli
139 1162 99.4 371 1 US-10-157-408-7 Sequence 7, Appli
140 1162 99.4 376 3 US-09-180-100-22 Sequence 22, Appli
141 1162 99.4 387 1 US-08-470-299-4 Sequence 4, Appli
142 1162 99.4 388 3 US-09-131-247-16 Sequence 16, Appli
143 1162 99.4 388 4 US-09-784-623-16 Sequence 16, Appli
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146 1162 99.4 394 4 US-09-854-864-31 Sequence 31, Appli
147 1162 99.4 396 2 US-08-784-512-3 Sequence 3, Appli
148 1162 99.4 397 3 US-09-176-228-3 Sequence 3, Appli
149 1162 99.4 397 4 US-09-854-864-18 Sequence 18, Appli
150 1162 99.4 398 4 US-09-612-033B-14 Sequence 14, Appli

ALIGNMENTS

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US-09-483-588-3
; Sequence 3, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Prestea
; TITLE OF INVENTION: Polypeptide Variance with Altered Effector Function
; FILE REFERENCE: P17261
; CURRENT APPLICATION NUMBER: US/09/483, 588
; EARLIER FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: US 60/116, 023
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-483-588-3

Query Match 99.9%; Score 1168; DB 4; Length 218;
Best Local Similarity 99.5%; Pred. No. 4.7e-114;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PABLLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV DGVENNAKT 60
DB 1 PABLLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV DGVENNAKT 60
QY 61 KPRBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKRTISKAKGQPREPQV 120
DB 61 KPRBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKRTISKAKGQPREPQV 120
QY 121 TLPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 180
DB 121 TLPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 180
QY 181 LTVDKSRWQCGNVFSCSYMEHAIHNYTQKSLISLSPGK 218
DB 181 LTVDKSRWQCGNVFSCSYMEHAIHNYTQKSLISLSPGK 218

RESULT 2
US-09-301-593-22
; Sequence 22, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saldanha, Jose W.
; TITLE OF INVENTION: RFP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301, 593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086, 049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-22

Query Match 99.9%; Score 1168; DB 4; Length 330;
Best Local Similarity 99.5%; Pred. No. 8.6e-114;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 113 PABLLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV DGVENNAKT 172
QY 61 KPRBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKRTISKAKGQPREPQV 120
DB 173 KPRBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKRTISKAKGQPREPQV 232
QY 121 TLPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 180
DB 233 TLPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 292
QY 181 LTVDKSRWQCGNVFSCSYMEHAIHNYTQKSLISLSPGK 218
DB 293 LTVDKSRWQCGNVFSCSYMEHAIHNYTQKSLISLSPGK 330

RESULT 3
US-08-775-066-2
; Sequence 2, Application US/08775066

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:17:31 ; Search time 125 Seconds
(without alignments)
674.510 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
Sequence: 1 PAELLGGPSVFLPPKPKD.....MHEALHHYTKSLSPK 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1168	99.9	218	8	ABR42438 Human IgG
6	1168	99.9	218	8	ADH75377 Human IgG
7	1168	99.9	223	6	ABG75664 Synagis h
8	1168	99.9	228	5	ABG32497 Human IgG
9	1168	99.9	232	3	AAV70251 Human imm
10	1168	99.9	232	3	AAV95579 Human imm
11	1168	99.9	232	4	AAAB49155 Human imm
12	1168	99.9	232	4	AAAB2642 Human imm
13	1168	99.9	232	5	ABR39643 Human IgG
14	1168	99.9	232	5	AAE28092 Human imm
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18	1168	99.9	264	6	AAE30921 Val8-GLP-
19	1168	99.9	264	6	AAE30923 Val8-GLP-
20	1168	99.9	272	6	AAE30922 Val8-GLP-
21	1168	99.9	272	6	AAE30924 Val8-GLP-
22	1168	99.9	272	6	AAE30925 Gly8-Glu2
23	1168	99.9	272	6	AAE30933 Exendin-4
24	1168	99.9	272	6	AAE30932 Exendin-4
25	1168	99.9	280	6	AAE30930 Gly8-Glu2

26	1168	99.9	287	6	AAE30934 Exendin-4
27	1168	99.9	287	6	AAE30926 Gly8-Glu2
28	1168	99.9	287	6	AAE30931 Gly8-Glu2
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30	1168	99.9	292	4	AAE02647 Human IgG
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32	1168	99.9	302	6	AAE30928 Human IgG
33	1168	99.9	329	8	ADH75387 Human IgG
34	1168	99.9	330	2	AAE50153 Human hea
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36	1168	99.9	330	7	ADJ94620 Human IgG
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38	1168	99.9	330	8	ADQ92917 Human IgG
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44	1168	99.9	385	8	ADL64008 Protein e
45	1168	99.9	385	8	ADL63969 Protein e
46	1168	99.9	394	8	ADL64009 Protein e
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56	1168	99.9	401	2	AAW10537 Leptin 1-
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ALIGNMENTS

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ID AAB07474 standard; protein; 218 AA.
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AC AAB07474;
XX
DT 20-OCT-2000 (first entry)
XX
DE Native IgG Fc region humIgG1 (non-A allotype).
XX
KW Igg antibody; light chain; Fc region; effector function; cancer; allergy;
XX asthma; LfA-1-mediated disorder; tumour; cancer.
OS Homo sapiens.
XX
PN WO200042072-A2.

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XX 20-JUL-2000.
PD 14-JAN-2000; 2000WO-US000973.
XX
PF 15-JAN-1999; 99US-0116023P.
XX
PR (GETH ) GENENTECH INC.
PA
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PI Presta LG;
XX
DR WPI; 2000-476035/41.
XX
PT New Fc region-containing polypeptides that have altered effector function
PT due to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX
PS Disclosure; Fig 22A; 132pp; English.
XX
CC AAB07474-78 represent native IgG Fc regions. The proteins are used to
CC produce Fc region-containing polypeptides that have altered effector
CC function as a consequence of one or more amino acid modifications in the
CC Fc region. The variant polypeptides are useful for treating cancer,
CC allergic conditions such as asthma (with an anti-IgE antibody), and LfA-1
CC -mediated disorders. Where the polypeptide binds the HER2 receptor, the
CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant
CC tumour characterized by overexpression of the HER2 receptor. Such cancers
CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-
CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer,
CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,
CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland
CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,
CC thyroid cancer, hepatic carcinoma and various types of head and neck
CC cancer
XX
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XX
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Best Local Similarity 99.5%; Pred. No. 3.1e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 PABELLGSPVFLFPKPKDITLISRPEVTCVVVDVSHEDPEVKENYVDGVEYNAKT 60
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DB 61 KRREQYKXTRVSVLTVLHQDWLNGKEYCKCKSNKLLPAPIETTSKAGQPREPQVY 120
QY 121 TLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTPPVLDSDGSFFLYSK 180
DB 121 TLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTPPVLDSDGSFFLYSK 180
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ID AAB76421 standard; protein; 218 AA.
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AC AAB76421;
XX
DT 10-APR-2001 (first entry)
XX
DE Human IgG1 non-A Fc region amino acid sequence.
XX
KW Human; erbb2; HER2; cancer; nervous system disease; stroke; ischaemia;
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
XX

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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:31:08 ; Search time 25 Seconds

(without alignments)
839.010 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.9	255	4 S31866	Ig gamma-1 chain C
2	1168	99.9	330	1 GHNU	Ig gamma-1 chain C
3	1162	99.4	374	2 S69339	Ig heavy chain V r
4	1122	96.0	234	2 PT0207	Ig gamma-3 chain C
5	1118	95.6	377	2 A23511	Ig gamma-3 chain C
6	1116	95.5	377	2 A60764	Ig gamma-3 chain C
7	1107	94.7	327	1 G4HU	Ig gamma-2 chain C
8	1106.5	94.7	326	1 G2HU	Ig gamma-2 chain C
9	1093	93.5	289	1 G3HWI	Ig gamma-3 heavy C
10	892	76.3	323	1 GHRB	Ig gamma-3 chain C
11	882	75.4	328	2 I47160	Ig gamma-2 chain C
12	882	75.4	328	2 I47159	Ig gamma-2 chain C
13	876	74.9	277	2 I47162	Ig gamma-2 chain C
14	859	73.5	329	1 G2GP	Ig gamma-2 chain C
15	856	73.2	328	2 I47158	Ig gamma-1 chain C
16	854	73.1	328	2 I47161	Ig gamma-3 chain C
17	835	71.4	470	2 S22080	Ig heavy chain pre
18	831	71.1	472	2 S31459	Ig gamma-1 chain C
19	831	71.1	472	2 S31459	Ig gamma-1 chain C
20	830	71.0	329	1 G3MSC	Ig gamma-3 chain C
21	819	70.1	358	1 G3MSM	Ig gamma-3 chain C
22	814	69.6	333	2 PS0018	Ig gamma-2b chain
23	811.5	69.4	444	2 PC4436	monoclonal antibod
24	810	69.3	326	2 PS0017	Ig gamma-1 chain C
25	801.5	68.6	324	1 G1MS	Ig gamma-1 chain C
26	800	68.4	329	2 S00847	Ig gamma-2c chain
27	796.5	68.1	393	1 G1MSM	Ig gamma-1 chain C
28	784	67.1	330	1 G2MSA	Ig gamma-2a chain
29	784	67.1	469	2 S37483	Ig gamma-2a chain

30	779	66.6	399	1 G2MSAM	Ig gamma-2a chain
31	778	66.6	322	2 PS0019	Ig gamma-2a chain
32	776	66.4	335	1 G2MSAB	Ig gamma-2a chain
33	769	65.8	446	2 S40295	Ig gamma-2a chain
34	760	65.0	327	2 S06611	Ig gamma-2 chain C
35	756	64.7	474	1 G2MS11	Ig gamma-2b chain
36	751	64.2	405	1 G2MSBM	Ig gamma-2b chain
37	751	62.8	475	2 S01321	Ig gamma-2b chain
38	703	60.1	180	2 I46732	Ig gamma heavy cha
39	576.5	49.3	249	2 S69340	Ig heavy chain V-I
40	574.5	49.1	218	2 A36040	Ig heavy chain V-I
41	567	48.5	152	2 S14236	Ig gamma-1 chain C
42	394	33.7	572	2 B46529	Ig heavy chain (
43	357	30.5	453	2 S37768	Ig mu chain C regi
44	356.5	30.5	549	2 S04845	Ig heavy chain pre
45	355.5	30.4	448	2 S03186	Ig heavy chain C r
46	355	30.4	391	1 MHHUT	Ig mu heavy chain
47	352	30.1	429	1 EHRT	Ig epsilon chain C
48	351	30.0	388	1 EHMS	Ig epsilon chain C
49	348.5	29.8	452	1 MHRU	Ig mu chain C regi
50	348	29.8	426	2 I36948	Ig epsilon-chain -
51	348	29.8	548	2 S38864	Ig epsilon chain C
52	347	29.7	428	1 EHRU	Ig epsilon chain C
53	347	29.7	627	2 S14683	Ig mu chain precu
54	346	29.6	343	2 S25644	Ig mu chain C regi
55	345	29.5	455	1 MHS	Ig mu chain C regi
56	345	29.5	455	2 A24976	Ig mu chain C regi
57	344	29.4	474	2 S15590	Ig heavy chain - h
58	338.5	29.0	473	1 MHHUM	Ig mu chain C regi
59	336.5	28.8	504	2 S00390	Ig gamma chain (cl
60	335	28.7	458	1 MHRB	Ig mu chain C regi
61	335	28.7	476	1 MHRSM	Ig mu chain C regi
62	331	28.3	450	1 MHDG	Ig mu chain C regi
63	329.5	28.2	423	1 EHMS	Ig epsilon chain C
64	327.5	28.0	112	2 B30503	Ig gamma-2a chain
65	327	28.0	454	1 MHRU	Ig mu chain C regi
66	325	27.8	479	1 MHRBM	Ig mu chain C regi
67	322	27.5	457	2 S03961	Ig mu chain C regi
68	321	27.5	592	2 S25705	Ig mu chain - shee
69	312	26.7	453	2 C31933	Ig mu chain C regi
70	296.5	25.4	433	2 S31436	Ig mu chain C regi
71	295	25.2	577	2 I50731	Ig heavy chain - n
72	294	25.1	438	1 HVRK2	Ig mu chain C regi
73	288.5	24.7	342	2 I47175	Ig alpha chain C r
74	286.5	24.5	367	1 MHCH	Ig mu chain C regi
75	281	24.0	438	1 HVRKCS	Ig mu chain C regi
76	277.5	23.7	349	1 AHRB	Ig alpha chain C r
77	277	23.7	343	2 S09272	Ig alpha chain - c
78	272.5	23.3	585	2 A46507	Ig mu chain C regi
79	272	23.3	461	1 HVRKCS	Ig mu chain C regi
80	272	23.3	461	1 HVRKCS	Ig mu chain C regi
81	271.5	23.2	88	2 A30503	Ig gamma-2b chain
82	271.5	23.2	338	2 S09276	Ig alpha chain C r
83	270	23.1	393	1 HVRK1	Ig mu chain C regi
84	268.5	23.0	684	2 S60266	novel antigen rece
85	267.5	22.9	339	2 S09264	Ig alpha chain C r
86	266.5	22.8	244	2 S12328	Ig heavy chain C r
87	266	22.8	357	2 S09269	Ig alpha chain C r
88	262	22.4	111	2 S43148	Ig epsilon chain -
89	260.5	22.3	357	2 S09265	Ig alpha chain C r
90	258.5	22.1	348	2 S09270	Ig alpha chain C r
91	258.5	22.1	352	2 S09266	Ig alpha chain C r
92	256.5	21.9	348	2 S09273	Ig alpha chain C r
93	255.5	21.9	340	2 I56230	Ig alpha-2 chain -
94	255.5	21.9	340	2 B23360	Ig alpha-2 chain C
95	255.5	21.9	347	2 S09274	Ig alpha chain C r
96	255	21.8	353	1 AIHU	Ig alpha chain C r
97	253.5	21.7	352	2 S05500	Ig alpha-1 chain C
98	253.5	21.7	474	2 I50830	Ig mu chain C regi
99	252.5	21.6	454	2 A46532	Ig mu chain C regi
100	252	21.6	360	2 S09271	Ig alpha chain C r
101	249	21.3	568	2 A34891	Ig heavy chain pre
102	246.5	21.1	340	1 A2HU	Ig alpha-2 chain C

103	246	21.0	342	2	A45966	Ig alpha chain C r
104	245.5	21.0	568	2	A45804	Ig mu chain C regi
105	245	21.0	220	2	C23260	Ig alpha-2 chain C
106	245	21.0	357	2	S09267	Ig alpha chain C r
107	241	20.6	573	2	S12838	Ig mu chain precu
108	238.5	20.4	344	1	AHMS	Ig alpha chain C r
109	237	20.3	580	2	A46538	Ig heavy chain, se
110	233	19.9	358	2	S09268	Ig alpha chain C r
111	230.5	19.7	335	2	S09275	Ig alpha chain C r
112	209	17.9	115	2	I68731	Ig epsilon chain C r
113	206	17.6	448	2	A46533	Ig heavy chain C r
114	203	17.4	402	2	S20002	Ig heavy chain, se
115	202	17.3	115	2	I68727	Ig epsilon chain C r
116	201	17.2	228	2	S03050	Ig gamma chain C1
117	191.5	16.4	140	2	A34509	Ig light chain C r
118	184.5	15.8	233	2	I51383	Ig lambda chain - s
119	184.5	15.8	240	2	A41797	Ig light chain - s
120	183.5	15.7	106	2	S22760	Ig lambda-2 chain
121	183.5	15.7	214	2	PC4156	Ig lambda chain V
122	183.5	15.7	1005	2	TI8537	Ig heavy chain - c
123	182	15.6	212	2	S70431	Ig lambda chain - c
124	181	15.5	102	2	B34509	Ig light chain C r
125	180	15.4	231	2	S25751	Ig lambda chain -
126	179	15.3	216	2	S03401	Ig lambda chain (K
127	179	15.3	509	2	JC5288	SHP substrate-1 pr
128	179	15.3	513	2	JC5289	SHP substrate-1 pr
129	178	15.2	105	2	B27390	Ig lambda-2 chain
130	178	15.2	227	2	PH1215	Ig epsilon chain C
131	178	15.2	243	2	PH1216	Ig epsilon chain C
132	177.5	15.2	105	1	LIMS	Ig lambda-1 chain
133	177	15.1	118	2	A46516	Ig lambda chain J-
134	175	15.0	118	2	A39949	Ig lambda chain C-
135	173	14.8	232	2	S25756	Ig lambda chain -
136	173	14.8	235	2	S25750	Ig lambda chain -
137	172	14.7	115	2	E53116	Ig epsilon chain C
138	172	14.7	118	2	C46516	Ig lambda chain C
139	171	14.6	118	2	S12440	Ig lambda chain (M
140	171	14.6	235	2	S25754	Ig lambda chain -
141	171	14.6	235	2	S25758	Ig lambda chain -
142	170.5	14.6	118	2	B30505	Ig lambda-6 chain
143	170.5	14.6	232	2	S17399	Ig lambda chain pr
144	170	14.5	118	2	S14443	Ig lambda chain (K
145	169.5	14.5	231	2	PC4155	Ig gamma-2b chain
146	169	14.5	105	2	S22762	Ig lambda-2 chain
147	169	14.5	231	2	S25738	Ig lambda chain -
148	168.5	14.4	234	2	S25757	Ig lambda chain -
149	168	14.4	235	2	S05270	Ig lambda chain pr
150	167	14.3	105	2	S22759	Ig lambda-2 chain

ALIGNMENTS

RESULT 1

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filipula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <Full>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C:Keywords: immunoglobulin

F:1-32/Region: Escherichia coli outer membrane protein A precursor

F:23-255/Region: human Ig gamma-1 chain C region

Query Match 99.9%; Score 1168; DB 4; Length 255;

Best Local Similarity 99.5%; Pred. No. 2,36-85;									
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	1	PAPILGSPVFLPPPKKOTLMSRTPEVTCVVVDVSHEDPEKFMVYDGVVNAKT	60						
Db	38	PAPILGSPVFLPPPKKOTLMSRTPEVTCVVVDVSHEDPEKFMVYDGVVNAKT	97						
Qy	61	KPREQYXKTVRVSVTLVTLHODWLNKGEYCKVSNALPAPIKRTISKAKQPREPOVY	120						
Db	98	KPREQYXKTVRVSVTLVTLHODWLNKGEYCKVSNALPAPIKRTISKAKQPREPOVY	157						
Qy	121	TLPPSRDELTKQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPVLDGSGFFLYSK	180						
Db	158	TLPPSRDELTKQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPVLDGSGFFLYSK	217						
Qy	181	LTVDKSRWQGNVSCSVMEHALNNHYTKSLSPCK	218						
Db	218	LTVDKSRWQGNVSCSVMEHALNNHYTKSLSPCK	255						

RESULT 2

GHMU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90564; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <Full>

A:Cross-references: UNIPROT:P01857; EMBL:Z17370

A:Note: this sequence has the Gln(17) alleotypic marker, 97-Lys, and the Gln(1) markers, A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113/235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, B.

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R', 98-135 <CUN>

A:Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Accession: B90564

A:Contents: Bu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, N', 196-197, D', 199-238, E', 240,

A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hillebrand, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

Igen Primarstruktur.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:26:52 ; Search time 112.5 Seconds

(without alignments)
992.296 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169
Sequence: 1 PAPELLGGPSVFLPPKPKD.....MHEALHNYTKSLSPGK 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.9	330	1	GCI_HUMAN
2	1168	99.9	465	2	O6GMX6
3	1168	99.9	466	2	O6IN78
4	1168	99.9	469	2	O7Z7P5
5	1168	99.9	470	2	O6BPA4
6	1168	99.9	470	2	O7Z5W1
7	1168	99.9	472	2	O6N089
8	1168	99.9	475	2	O6GMW7
9	1168	99.9	476	2	O6GMX1
10	1168	99.9	679	2	O96P08
11	1164	99.6	473	2	O6P055
12	1164	99.6	475	2	O6M2Q6
13	1164	99.6	480	2	O6N094
14	1164	99.6	481	2	O6N097
15	1164	99.6	482	2	O7Z351
16	1163	99.5	487	2	O65ZL2
17	1162	99.4	348	2	O6PYX1
18	1162	99.4	473	2	O6MZV7
19	1162	99.4	478	2	O6P181
20	1162	99.4	480	2	O6PJF1
21	1161	99.3	466	2	O6N096
22	1157	99.0	475	2	O6N095
23	1157	99.0	544	2	O6P095
24	1118	95.6	354	2	O6BT22
25	1118	95.6	518	2	O6N030
26	1114	95.3	521	2	O8N4Y9
27	1107	94.7	427	1	GCA_HUMAN
28	1107	94.7	433	1	O8TC63
29	1106.5	94.7	326	1	GCI_HUMAN
30	1106.5	94.7	417	2	O6N093
31	1103.5	94.4	464	2	O6MZU6

32	1103	94.4	509	2	O8NP17	O8NF17 homo sapien
33	1101.5	94.2	465	2	O6P6C4	O6P6C4 homo sapien
34	1098	93.9	290	1	GCI_HUMAN	P01860 homo sapien
35	1098	93.9	476	2	O6MZX7	O6MZX7 homo sapien
36	1092.5	93.5	493	2	O6BCK4	O6BCK4 homo sapien
37	892	76.3	323	1	GC_RABIT	P01870 oryctolagus
38	861	75.4	337	2	O9SM34	O9SM34 equus caball
39	859	72.5	329	1	GC2_CAVPO	P01862 cavia porce
40	830	71.0	329	1	GC3_MOUSE	P22436 mus musculus
41	830	71.0	470	2	O7TMK1	O7TMK1 mus musculus
42	819	70.1	303	2	O6KAM2	O6KAM2 mus musculus
43	819	70.1	398	1	GC3M_MOUSE	P03987 mus musculus
44	814	69.6	333	1	GCB_RAT	P20761 rattus norv
45	812.5	69.5	463	2	O991C4	O991C4 mus musculus
46	811.5	69.4	458	2	O65ZQ1	O65ZQ1 homo sapien
47	810	69.3	326	1	GCI_RAT	P20759 rattus norv
48	801.5	68.6	324	1	GCI_MOUSE	P01868 mus musculus
49	800	68.4	329	1	GCC_RAT	P20762 rattus norv
50	796.5	68.1	393	1	GCIM_MOUSE	P01869 mus musculus
51	784	67.1	330	1	GCIA_MOUSE	P01863 mus musculus
52	784	67.1	464	2	O6PF95	O6PF95 mus musculus
53	780	66.7	464	2	O6PIP8	O6PIP8 mus musculus
54	780	66.7	465	2	O6P1B2	O6P1B2 mus musculus
55	780	66.7	471	2	O6EK04	O6EK04 mus musculus
56	780	66.7	472	2	O6PUA7	O6PUA7 mus musculus
57	779	66.6	399	1	GCAM_MOUSE	P01865 mus musculus
58	778	66.6	322	1	GCA_RAT	P20760 rattus norv
59	776	66.4	335	1	GCAB_MOUSE	P01864 mus musculus
60	776	66.4	473	2	O9D814	O9D814 mus musculus
61	757	64.8	473	2	O91Z05	O91Z05 mus musculus
62	757	64.8	474	2	O8R3H6	O8R3H6 mus musculus
63	756	64.7	336	1	GCB_MOUSE	P01866 mus musculus
64	751	64.2	405	1	GCBM_MOUSE	P01867 mus musculus
65	357	30.5	375	2	O8BET1	O8BET1 homo sapien
66	357	30.5	454	1	MIC_HUMAN	P01871 homo sapien
67	357	30.5	597	2	O96BB9	O96BB9 homo sapien
68	357	30.5	597	2	O6GMX5	O6GMX5 homo sapien
69	357	30.5	597	2	O9B0B8	O9B0B8 homo sapien
70	357	30.5	597	2	O9BU10	O9BU10 homo sapien
71	357	30.5	606	2	O6GMV2	O6GMV2 homo sapien
72	355	30.4	391	1	MICB_HUMAN	P04220 homo sapien
73	354.5	30.3	585	2	O6GPX4	O6GPX4 xenopus lae
74	352	30.1	429	1	EPG_RAT	P01855 rattus norv
75	351	29.8	584	2	EPIC_MOUSE	P06336 mus musculus
76	348.5	29.8	584	2	O6INK3	O6INK3 xenopus lae
77	347	29.7	428	1	EPIC_HUMAN	P01854 homo sapien
78	347	29.7	595	2	O8WUX4	O8WUX4 homo sapien
79	347	29.7	613	2	O8WUK1	O8WUK1 homo sapien
80	347	29.7	620	2	O96EY0	O96EY0 homo sapien
81	347	29.7	625	2	O96AA6	O96AA6 homo sapien
82	345	29.5	455	1	MIC_MOUSE	P01872 mus musculus
83	337	28.8	614	2	O7TMT6	O7TMT6 mus musculus
84	335	28.7	458	1	MIC_RABIT	P03988 oryctolagus
85	335	28.7	476	1	MICM_MOUSE	P01873 mus musculus
86	335	28.7	613	2	O8VCX7	O8VCX7 mus musculus
87	331	28.3	450	1	MIC_CANFA	P01874 canis famli
88	325	27.8	459	1	MICM_RABIT	P04221 oryctolagus
89	324	27.7	454	1	MIC_MESAU	P06331 mesocricetu
90	322	27.5	457	1	MIC_SUNMU	P20768 sunus murt
91	315	26.9	572	2	O6107	O6107 xenopus lae
92	312	26.7	587	2	O7TOR1	O7TOR1 xenopus lae
93	312	26.7	588	2	O61R66	O61R66 xenopus lae
94	312	26.7	593	2	O61NMS	O61NMS xenopus lae
95	312	26.7	605	2	O6GNB3	O6GNB3 xenopus lae
96	306	26.2	614	2	O6DD07	O6DD07 xenopus lae
97	294	25.1	438	1	HVC2_HETPR	P23085 heterodontu
98	286.5	24.5	446	1	HVC3_CHICK	P01875 gallus gall
99	281	24.0	438	1	HVC5_HETPR	P23087 heterodontu
100	277.5	23.7	299	1	ALC_RABIT	P01879 oryctolagus
101	272	23.3	370	1	HVC1_HETPR	P23084 heterodontu
102	272	23.3	461	1	HVC3_HETPR	P23088 heterodontu
103	270	23.1	393	1	HVC3_HETPR	P23086 heterodontu
104	268.5	23.0	684	2	O90544	O90544 ginglymosco

105	257.5	22.0	478	2	Q7Z379	Q7Z379	homo sapien
106	257.5	22.0	492	2	Q7Z374	Q7Z374	homo sapien
107	255.5	21.9	340	1	ALC2 HUMAN	P01877	homo sapien
108	255.5	21.9	416	2	Q9NP66	Q9NP66	homo sapien
109	255.5	21.9	477	2	Q6CMK7	Q6CMK7	homo sapien
110	255.5	21.9	478	2	Q6MYH3	Q6MYH3	homo sapien
111	255.5	21.9	479	2	Q6MZV6	Q6MZV6	homo sapien
112	255.5	21.9	480	2	Q6P089	Q6P089	homo sapien
113	255.5	21.9	483	2	Q6MZK9	Q6MZK9	homo sapien
114	255.5	21.9	487	2	Q6ZYX0	Q6ZYX0	homo sapien
115	255	21.8	353	1	ALC1 HUMAN	P01876	homo sapien
116	255	21.8	384	2	Q9UP60	Q9UP60	homo sapien
117	255	21.8	493	2	Q8NCL6	Q8NCL6	homo sapien
118	255	21.8	493	2	Q6GMX2	Q6GMX2	homo sapien
119	255	21.8	494	2	Q6KXK8	Q6KXK8	homo sapien
120	255	21.8	496	2	Q6KXK8	Q6KXK8	homo sapien
121	255	21.8	506	2	Q6KXK8	Q6KXK8	homo sapien
122	255	21.8	506	2	Q6N090	Q6N090	homo sapien
123	254.5	21.8	498	2	Q6N041	Q6N041	homo sapien
124	254.5	21.8	500	2	Q6N091	Q6N091	homo sapien
125	253.5	21.7	353	1	ALC1 GORGO	P20758	gorilla gor
126	252	21.6	494	2	Q6ZM64	Q6ZM64	homo sapien
127	252	21.6	496	2	Q6ZM64	Q6ZM64	homo sapien
128	252	21.6	499	2	Q8NSK4	Q8NSK4	homo sapien
129	252	21.6	519	2	Q6N092	Q6N092	homo sapien
130	250	21.4	497	2	Q8WY24	Q8WY24	homo sapien
131	250	21.4	500	2	Q8WY24	Q8WY24	homo sapien
132	245.5	21.0	481	1	MUCM ICTRU	P23735	ictalurus p
133	241.5	20.7	481	2	Q91WT1	Q91WT1	mus musculus
134	241.5	20.7	481	2	Q91WT3	Q91WT3	mus musculus
135	241.5	20.7	482	2	Q91X92	Q91X92	mus musculus
136	241.5	20.7	482	2	Q8K172	Q8K172	mus musculus
137	241.5	20.7	484	2	Q8VEA0	Q8VEA0	mus musculus
138	241.5	20.7	485	2	Q6PDB8	Q6PDB8	mus musculus
139	241.5	20.7	487	2	Q80Z17	Q80Z17	mus musculus
140	241.5	20.7	488	2	Q8K0F2	Q8K0F2	mus musculus
141	241.5	20.7	488	2	Q91MR1	Q91MR1	mus musculus
142	241.5	20.7	489	2	Q8VCX4	Q8VCX4	mus musculus
143	239.5	20.5	479	2	Q91WPS	Q91WPS	mus musculus
144	238.5	20.4	344	1	ALC1 MOUSE	P01878	mus musculus
145	238.5	20.4	479	2	Q91W22	Q91W22	mus musculus
146	238.5	20.4	479	2	Q7TMK4	Q7TMK4	mus musculus
147	238.5	20.4	480	2	Q91XEL	Q91XEL	mus musculus
148	238.5	20.4	480	2	Q8K0Z4	Q8K0Z4	mus musculus
149	238.5	20.4	481	2	Q8VCV5	Q8VCV5	mus musculus
150	238.5	20.4	484	2	Q991A6	Q991A6	mus musculus

ALIGNMENTS

RESULT 1
GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 19 gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.D., Hood L.B.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene."
RL Nucleic Acids Res. 10:4071-4079 (1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Maxam A.M., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170 (1970).
[3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181 (1970).
[4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponsing H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
[5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
[6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196 (1970).
[7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Delsenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from *Staphylococcus*
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370 (1981).
[9]
RP MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
CC GIM(1) marker, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
[10]
RP MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
[11]
RP MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
[12]
RP MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
[13]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
DR EMBL/J00028; AAC82527.1; ALT_INIT.

DR PIR; A93433; GHMU.
 DR PDB; 1A7; X-ray; H=1-103.
 DR PDB; 1D5B; X-ray; B/H=1-101.
 DR PDB; 1D5I; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FCL; X-ray; A/B=106-329.
 DR PDB; 1FCJ; X-ray; D=106-329.
 DR PDB; 1FCJ; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I17; X-ray; B/D=1-103.
 DR PDB; 1I1S; X-ray; A/B=107-330.
 DR PDB; 1I1X; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1LOK; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; .
 DR GO; GO:0005624; C:membrane fraction; NMS.
 DR GO; GO:0003823; P:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_1ike.
 DR InterPro; IPR003066; IG_MHC.
 DR Pfam; PF00047; IG_3.
 DR PROSITE; PSS0835; IG_LIKE; 3.
 DR PROSITE; PSS0290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
 KM
 FT NON_TER 1 1
 FT DOMAIN 98 98 CH1.
 FT DOMAIN 99 110 Hinge.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISUFID 27 83 Interchain (with light chain).
 FT DISUFID 103 103 Interchain (with heavy chain).
 FT DISUFID 109 109 Interchain (with heavy chain).
 FT DISUFID 112 112 Interchain (with heavy chain).
 FT DISUFID 144 204
 FT DISUFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97
 FT
 FT VARIANT 239 239 N-linked (GlcNAc...).
 FT
 FT VARIANT 241 241 K -> R (in GIM(3) marker).
 FT
 FT VARIANT 241 241 /FTId=VAR_003886.
 FT
 FT VARIANT 241 241 D -> E (in GIM(non-1) marker).
 FT
 FT VARIANT 241 241 /FTId=VAR_003887.
 FT
 FT VARIANT 241 241 L -> M (in GIM(non-1) marker).
 FT
 FT VARIANT 241 241 /FTId=VAR_003888.
 FT
 FT STRAND 23 24
 FT STRAND 26 33
 FT STRAND 38 38
 FT STRAND 41 41
 FT TURN 42 45
 FT TURN 48 49
 FT STRAND 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT STRAND 73 75
 FT HELIX 76 78
 FT TURN 82 87
 FT STRAND 88 91
 FT TURN 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT STRAND 130 134
 FT HELIX 136 137
 FT TURN 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 177 177
 FT TURN 179 180

FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 238 242
 FT HELIX 245 256
 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 311
 FT TURN 313 314
 FT HELIX 316 318
 FT STRAND 319 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2FA33D CRC64;
 Query Match 99.9%; Score 1168; DB 1; Length 330;
 Best Local Similarity 99.5%; Pred. No. 5,5e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PAPELLGSPVLPFPKPKDTLMISRTPEVTCVVDVSHEDPEKFNMYVDVGVVNAKT 60
 DB 113 PAPELLGSPVLPFPKPKDTLMISRTPEVTCVVDVSHEDPEKFNMYVDVGVVNAKT 172
 QY 61 KPREEQYNKYRVSVLTIVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVY 120
 DB 173 KPREEQYNKYRVSVLTIVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVY 232
 QY 121 TLPPSRDELTKQVSLTCLVKGFPYPSDIAVEMESNQPENNYKTPPVLDSDGSPFLYSK 180
 DB 233 TLPPSRDELTKQVSLTCLVKGFPYPSDIAVEMESNQPENNYKTPPVLDSDGSPFLYSK 292
 QY 181 LITDKSRMOQGNVFCSCVNHVHVALHNHYTQKSLSLSPGK 218
 DB 293 LITDKSRMOQGNVFCSCVNHVHVALHNHYTQKSLSLSPGK 330
 RESULT 2
 Q6GMX6 PRELIMINARY; PRT; 465 AA.
 AC Q6GMX6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spletton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073766; AAH73766.1; --
 DR InterPro; IPR003599; IG_1-like.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_1-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00654; Cl-set; 3.
 DR Pfam; PF00654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
 SQ

Query Match 99.9%; Score 1168; DB 2; Length 465;
 Best Local Similarity 99.5%; Pred. No. 8.3e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPERLGGPSVFLPPPKKDTMTSRTPVTCVVVDVSHEDPEVKFNNYVDSGEVYHNAKT 60
 Db 248 PAPERLGGPSVFLPPPKKDTMTSRTPVTCVVVDVSHEDPEVKFNNYVDSGEVYHNAKT 307
 QY 61 KPREQYNXKTYRVSVLTVLHQDLNIGKEPKCKVSNKALPAPIETKISKAKGQPREPOVY 120
 Db 308 KPREQYNXKTYRVSVLTVLHQDLNIGKEPKCKVSNKALPAPIETKISKAKGQPREPOVY 367
 QY 121 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
 Db 368 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 427
 QY 181 LTVDKSRWQOGNVPSCVMHEALHNHYTQKSLSLSPGK 218
 Db 428 LTVDKSRWQOGNVPSCVMHEALHNHYTQKSLSLSPGK 465

RESULT 3

Q6IN78 PRELIMINARY; PRT; 466 AA.
 AC Q6IN78;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxId=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shewen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Caminici P., Prange C.,
 RA Raha S.S., Loguano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bonak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal Nervous System;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; --
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_1-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00654; Cl-set; 3.
 DR Pfam; PF00654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR SEQUENCE 466 AA; 50853 MW; 53EB0BCED81076E CRC64;
 SQ

Query Match 99.9%; Score 1168; DB 2; Length 466;
 Best Local Similarity 99.5%; Pred. No. 8.3e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPERLGGPSVFLPPPKKDTMTSRTPVTCVVVDVSHEDPEVKFNNYVDSGEVYHNAKT 60
 Db 249 PAPERLGGPSVFLPPPKKDTMTSRTPVTCVVVDVSHEDPEVKFNNYVDSGEVYHNAKT 308
 QY 61 KPREQYNXKTYRVSVLTVLHQDLNIGKEPKCKVSNKALPAPIETKISKAKGQPREPOVY 120
 Db 309 KPREQYNXKTYRVSVLTVLHQDLNIGKEPKCKVSNKALPAPIETKISKAKGQPREPOVY 368
 QY 121 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
 Db 369 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 428
 QY 181 LTVDKSRWQOGNVPSCVMHEALHNHYTQKSLSLSPGK 218
 Db 429 LTVDKSRWQOGNVPSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 4

Q7Z7P5 PRELIMINARY; PRT; 469 AA.
 AC Q7Z7P5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHG1 protein.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxId=9606;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shewen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,